



SEQUENCE LISTING

<110> AFAR, Daniel E. H.
HUBERT, Rene S.
LEONG, Kahan
RAITANO, Arthur B.
SAFFRAN, Douglas C.

<120> NOVEL PROSTATE-RESTRICTED GENE EXPRESSED
IN PROSTATE CANCER

<130> 511582001300

<140> US 09/547,788
<141> 2000-04-12

<150> US 60/128,860
<151> 1999-04-12

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3051
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (163) . . . (1365)

<400> 1
gacgcgtggg cgcggaggcg ctggggcgac ggcgcggagc cggccggagc tcgaggccgg
60
cggcggcggg agagcgaccc gggcggcctc gtagcggggc cccggatccc cgagtggcgg
120
ccggagcctc gaaaagagat tctcagcgct gatttgaga tg atg ggc ttg gga
174

Met Gly Leu Gly
1

aac ggg cgt cgc agc atg aag tcg ccg ccc ctc gtg ctg gcc gcc ctg
222
Asn Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu
5 10 15 20

gtg gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc
270
Val Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser
25 30 35

cgg agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc
318
Arg Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val
40 45 50

cgc agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag
 366
 Arg Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu
 55 60 65

 ttc cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag
 414
 Phe Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln
 70 75 80

 tcc agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac
 462
 Ser Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp
 85 90 95 100

 gaa aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc
 510
 Glu Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile
 105 110 115

 cga gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg
 558
 Arg Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg
 120 125 130

 ctg cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag
 606
 Leu Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu
 135 140 145

 agg aag ttc tcc tac gac ctg agc cag tgc atc aat cag atg aag gag
 654
 Arg Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
 150 155 160

 gtg aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg
 702
 Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly
 165 170 175 180

 aat gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga
 750
 Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg
 185 190 195

 cag cag ctc caa gcc ctc agt gag cct cag ccc agg ctg cag gca gca
 798
 Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala
 200 205 210

 ggc ctg cca cac aca gag gtg cca caa ggg aag gga aac gtg ctt ggt
 846
 Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly
 215 220 225

aac agc aag tcc cag aca cca gcc ccc agt tcc gaa gtg gtt ttg gat
894
Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp
230 235 240

tca aag aga caa gtt gag aaa gag gaa acc aat gag atc cag gtg gtg
942
Ser Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val
245 250 255 260

aat gag gag cct cag agg gac agg ctg ccg cag gag cca ggc cg^g gag
990
Asn Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu
265 270 275

cag gtg gtg gaa gac aga cct gta ggt gga aga ggc ttc ggg gga gcc
1038
Gln Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Ala
280 285 290

gga gaa ctg ggc cag acc cca cag gtg cag gct gcc ctg tca gtg agc
1086
Gly Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser Val Ser
295 300 305

cag gaa aat cca gag atg gag ggc cct gag cga gac cag ctt gtc atc
1134
Gln Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile
310 315 320

ccc gac gga cag gag gag cag gaa gct gcc ggg gaa ggg aga aac
1182
Pro Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn
325 330 335 340

cag cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa
1230
Gln Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu
345 350 355

gca gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga
1278
Ala Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg
360 365 370

aac ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat
1326
Asn Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn
375 380 385

tta ctt gat cag cgt gaa aag cg^g aat cat aca ctc tga attgaactgg
1375
Leu Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *
390 395 400

aatcacatat ttccacaacag ggccgaagag atgactataa aatgttcatg agggactgaa
1435

tactgaaaac tgtgaaatgt actaaataaa atgtacatct gaagatgatt attgtaaaat
1495
tttagtatgc actttgtgta ggaaaaaaatg gaatggtctt ttaaacagct tttggggggt
1555
actttgaaag tgtctaataa ggtgtcacaa tttttggtag taggtatttc gtgagaagtt
1615
caacaccaaa actggaacat agttctcctt caagtgttgg cgacagcggg gcttcctgat
1675
tctgaaatat aactttgtgt aaattaacag ccacctataag aagagtccat ctgctgtgaa
1735
ggagagacag agaactctgg gttccgtcgt cctgtccacg tgctgtacca agtgcgtgg
1795
ccagcctgtt acctgttctc actgaaaagt ctggctaatg ctcttgcgtta gtcacttctg
1855
attctgacaa tcaatcaatc aatggcctag agcactgact gttaacacaa acgtcactag
1915
caaagtagca acagctttaa gtctaaatac aaagctgttc tgtgtgagaa ttttttaaaa
1975
ggctacttgt ataataaccc ttgtcatttt taatgtacaa aacgctttaa agtggcttag
2035
aatttgaaca tttgtggctt ttatttactt tgcttcgtgt gtgggcaaag caacatctc
2095
cctaaatata tattaccaag aaaagcaaga agcagattag gttttgaca aaacaaacag
2155
gccaaaaggg ggctgacctg gagcagagca tggtagagg caaggcatga gagggcaagt
2215
ttgttgcgtt cagatctgtg cctactttt tactggagta aaagaaaaca aagttcattt
2275
atgtcgaagg atatatacag tgtagaaat taggactgtt tagaaaaaca ggaataacaat
2335
ggttgtttt atcatagtgt acacattttt cttgtggtaa atgactcaca aaactgattt
2395
taaaatcaag ttaatgtgaa ttttggaaat tactacttaa tcctaattca caataacaat
2455
ggcattaagg tttgacttga gttgggtctt agtattttt atggtaaataa ggctttacc
2515
acttgcaaat aactggccac atcattaatg actgacttcc cagtaaggct ctctaagggg
2575
taagtaggag gatccacagg attttagatg ctaaggcccc agagatcggt tgatccaacc
2635
ctcttatttt cagagggaa aatggggctt agaagttaca gagcatctag ctggtgcgct
2695
ggcacccctg gcctcacaca gactcccgag tagctggac tacaggcaca cagtcactga
2755
agcaggccct gtttgcattt cacgttgcca cctccaactt aaacattttt catatgtgt
2815
gtccttagtc actaagggtt aactttccca cccagaaaag gcaactttaga taaaatctta
2875
gagtttttc atactttctt aagtccttcc ccagcctcac tttgagtcct cttgggggt
2935
gataggaatt ttctcttgct ttctcaataa agtctctatt catctcatgt ttaatttgta
2995
cgcatagaat tgctgagaaa taaaatgttc tggtaactt aaaaaaaaaa aaaaaaa
3051

<210> 2
<211> 400

<212> PRT

<213> Homo sapien

<220>

<221> SIGNAL

<222> (1) ... (29)

<400> 2

Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val
1 5 10 15
Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp
20 25 30
Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu
35 40 45
Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu
50 55 60
Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu
65 70 75 80
Asp Lys Ile Gln Ser Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys
85 90 95
Leu Tyr Gln Asp Glu Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly
100 105 110
Glu Arg Leu Ile Arg Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg
115 120 125
Asn Tyr Gly Arg Leu Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln
130 135 140
Thr Asn Leu Glu Arg Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn
145 150 155 160
Gln Met Lys Glu Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val
165 170 175
Thr Lys Lys Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn
180 185 190
Asn Asp Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg
195 200 205
Leu Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
210 215 220
Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu
225 230 235 240
Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu
245 250 255
Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu
260 265 270
Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly
275 280 285
Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala
290 295 300
Leu Ser Val Ser Gln Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp
305 310 315 320
Gln Leu Val Ile Pro Asp Gly Gln Glu Glu Gln Glu Ala Ala Gly
325 330 335
Glu Gly Arg Asn Gln Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met
340 345 350
Asp Glu Asn Glu Ala Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala
355 360 365
Gly Asn Asp Arg Asn Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg
370 375 380
Asp Thr Ile Asn Leu Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu

385

390

395

400

<210> 3
<211> 4
<212> PRT
<213> Homo sapien

<400> 3
Asn Ile Thr Thr
1

<210> 4
<211> 4
<212> PRT
<213> Homo sapien

<400> 4
Asn Gln Thr Asn
1

<210> 5
<211> 4
<212> PRT
<213> Homo sapien

<400> 5
Asn His Thr Leu
1

<210> 6
<211> 4
<212> PRT
<213> Homo sapien

<400> 6
Arg Lys Phe Ser
1

<210> 7
<211> 4
<212> PRT
<213> Homo sapien

<400> 7
Lys Arg Asp Thr
1

<210> 8
<211> 4
<212> PRT
<213> Homo sapien

<400> 8
Thr Thr Gly Glu
1

<210> 9

<211> 4
<212> PRT
<213> Homo sapien

<400> 9
Thr Asn Leu Glu
1

<210> 10
<211> 4
<212> PRT
<213> Homo sapien

<400> 10
Ser Glu Thr Asp
1

<210> 11
<211> 8
<212> PRT
<213> Homo sapien

<400> 11
Lys Leu Arg Gly Glu Asp Asp Tyr
1 5

<210> 12
<211> 6
<212> PRT
<213> Homo sapien

<400> 12
Gly Leu Gly Asn Gly Arg
1 5

<210> 13
<211> 6
<212> PRT
<213> Homo sapien

<400> 13
Gly Leu Pro His Thr Glu
1 5

<210> 14
<211> 6
<212> PRT
<213> Homo sapien

<400> 14
Gly Asn Val Leu Gly Asn
1 5

<210> 15
<211> 6
<212> PRT
<213> Homo sapien

<400> 15
Gly Asn Ser Lys Ser Gln
1 5

<210> 16
<211> 6
<212> PRT
<213> Homo sapien

<400> 16
Gly Asn Asp Arg Asn Ile
1 5

<210> 17
<211> 4
<212> PRT
<213> Homo sapien

<400> 17
Asn Gly Arg Arg
1

<210> 18
<211> 14
<212> DNA
<213> Homo sapien

<400> 18
ttttgatcaa gctt
14

<210> 19
<211> 42
<212> DNA
<213> Homo sapien

<400> 19
ctaatacgac tcactatagg gctcgagcgg ccggccgggc ag
42

<210> 20
<211> 12
<212> DNA
<213> Homo sapien

<400> 20
ggcccggtcct ag
12

<210> 21
<211> 40
<212> DNA
<213> Homo sapien

<400> 21

gtaatacgac tcactatagg gcagcggt cgccggccgag
40

<210> 22
<211> 10
<212> DNA
<213> Homo sapien

<400> 22
cggttcctag
10

<210> 23
<211> 22
<212> DNA
<213> Homo sapien

<400> 23
ctaatacgac tcactatagg gc
22

<210> 24
<211> 22
<212> DNA
<213> Homo sapien

<400> 24
tcgagcgcc gcccggcag ga
22

<210> 25
<211> 20
<212> DNA
<213> Homo sapien

<400> 25
agcgtggtcg cggccgagga
20

<210> 26
<211> 25
<212> DNA
<213> Homo sapien

<400> 26
atatcgccgc gctcgtcgta gacaa
25

<210> 27
<211> 26
<212> DNA
<213> Homo sapien

<400> 27
agccacacgc agtcattgt agaagg
26

<210> 28
<211> 21
<212> DNA
<213> Homo sapien

<400> 28
tgtacacatt tagttgtgg t
21

<210> 29
<211> 25
<212> DNA
<213> Homo sapien

<400> 29
gccagttatt tgcaagtgg aagag
25

<210> 30
<211> 15
<212> PRT
<213> Homo sapien

<400> 30
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu
1 5 10 15